

Evolution Lab

In this lab you will practice graphing, hypothesis testing, statistical analysis and the mechanisms of evolution you have learned. Be sure to save this lab as it contains instructions for performing certain tasks needed for future labs.

Part 1

The warbler finch eats seeds for the main part of its diet. A scientist wanted to research how the seed characteristics influenced the finch's evolution. Finches with thicker beaks are more able to crack open harder seeds than those with thinner beaks. High precipitation tends to make seeds develop softer than areas with low precipitation which produce hard seeds. 2 different samples of finches were captured from 2 population sites, A & B, their beaks were measured, and then they were released back to their appropriate location. The data tables below represent the data collected by the scientist:

Table 1: Population Site A sample data
Set 1 of beak thickness in mm

4.99	5.10	5.21
4.99	5.12	5.26
5.01	5.14	5.30
5.06	5.18	5.36
5.09	5.19	5.37

SD 0.54 SE _____

Mean _____

Table 2: Population Site A sample data
Set 2 of beak thickness in mm

3.15	5.14	5.24
5.09	5.15	5.29
5.11	5.23	5.31
5.11	5.23	5.32
5.12	5.24	5.32

SD 0.12 SE _____

Mean _____

Table 3: Population Site B sample data
Set 1 of beak thickness in mm

7.24	7.25	7.29
7.24	7.26	7.29
7.24	7.28	7.30
7.25	7.28	7.31
7.25	7.28	7.31

SD 0.07 SE _____

Mean _____

Table 4: Population Site B sample data
Set 2 of beak thickness in mm

7.02	7.13	7.23
7.11	7.13	7.23
7.11	7.13	7.24
7.12	7.15	7.24
7.12	7.16	7.26

SD 0.03 SE _____

Mean _____

Graphing & Error Bars

1. Calculate the standard error (SE) & mean for each data set above.
2. Plot the two “**Site A**” sample sets’ means and error bars on graph paper by doing the following:
 - a. Plot a point for the set 1 mean.
 - b. Draw a vertical line above the mean point that is up the value of the SE; i.e. If the mean is 5.40 and the SE is 0.12, draw a vertical line from the mean point up 0.12 units until at 5.52 (mean + SE)
 - c. Repeat for a vertical line below the mean, minus the SE; i.e. If the mean is 5.40 and the SE is 0.12, draw a vertical line from the mean point down 0.12 units until at 5.28 (mean - SE).
 - d. Complete the error bars by putting a horizontal line intersecting the ends of the error bar.
 - e. Repeat for the set 2 mean.
3. Repeat step 2 for the two “**Site B**” sample sets.
4. Provide titles, axes labels with units and legends if needed.
5. For the site A data sets, decide if they are similar enough to be considered reliable estimates of the true population mean. If the error bars show overlap, it shows the two means are not significantly different and we can assume they are reliable estimates of the true population mean. No overlap means they are significantly different and not reliable estimates of the true mean.
6. Repeat step 5 for the site B data.
7. Under each graph explain your reliability decision from steps 5/6.

Null Hypothesis Testing by the t-test

A t-test is used to determine if 2 data sets are statistically different from each other. The results of a t-test give a number called the **p-value**, which tells us the probability that the data are different by chance alone. Any value greater than .05 is too high and we would conclude our data are similar just by chance, rather than by some scientific explanation. Values less than or equal to .05 are considered valid and mean there is a difference in our data that is significant.

A null hypothesis is stated in various forms but always ascertains that there will not be a significant difference in data. If the data are significantly different based on the t-test, we make a final decision to reject the null hypothesis. If data are not significantly different based on the t-test, we would accept the null hypothesis. Either way the results need a proposed biological explanation to conclude your results.

1. Write a null hypothesis concerning the 2 sample sets for population A.
2. Use the provided website to enter your data and record the p-value below.
http://www.physics.csbsju.edu/stats/t-test_bulk_form.html

3. Make a decision about the null hypothesis and explain your results. Keep in mind we are hoping these are statistically similar, meaning there is no difference statistically if $p > .05$.

4. Repeat for population B.

5. Write a null hypothesis comparing populations A and B. Decide how to pick data for the t-test, perform the t-test and explain your results.

Part 2

Table 1 – Moth Population “A” over 40 years in Costa Rica

	1975	1980	1985	1990	1995	2000	2005	2010	2015
Population Size	100,000	100,254	256	268	374	445	613	892	929
Allele B %	50%	53%	2%	27%	52%	63%	28%	35%	64%
Allele b %	50%	47%	98%	73%	48%	37%	72%	65%	36%

Table 2 – Moth Population “B” over 40 years in Ireland

	1975	1980	1985	1990	1995	2000	2005	2010	2015
Population Size	100,000	100,254	100,429	100,103	100,642	101,255	101,298	102,055	102,845
Allele B %	50%	53%	57%	59%	67%	74%	78%	83%	91%
Allele b %	50%	47%	43%	41%	33%	26%	22%	17%	9%

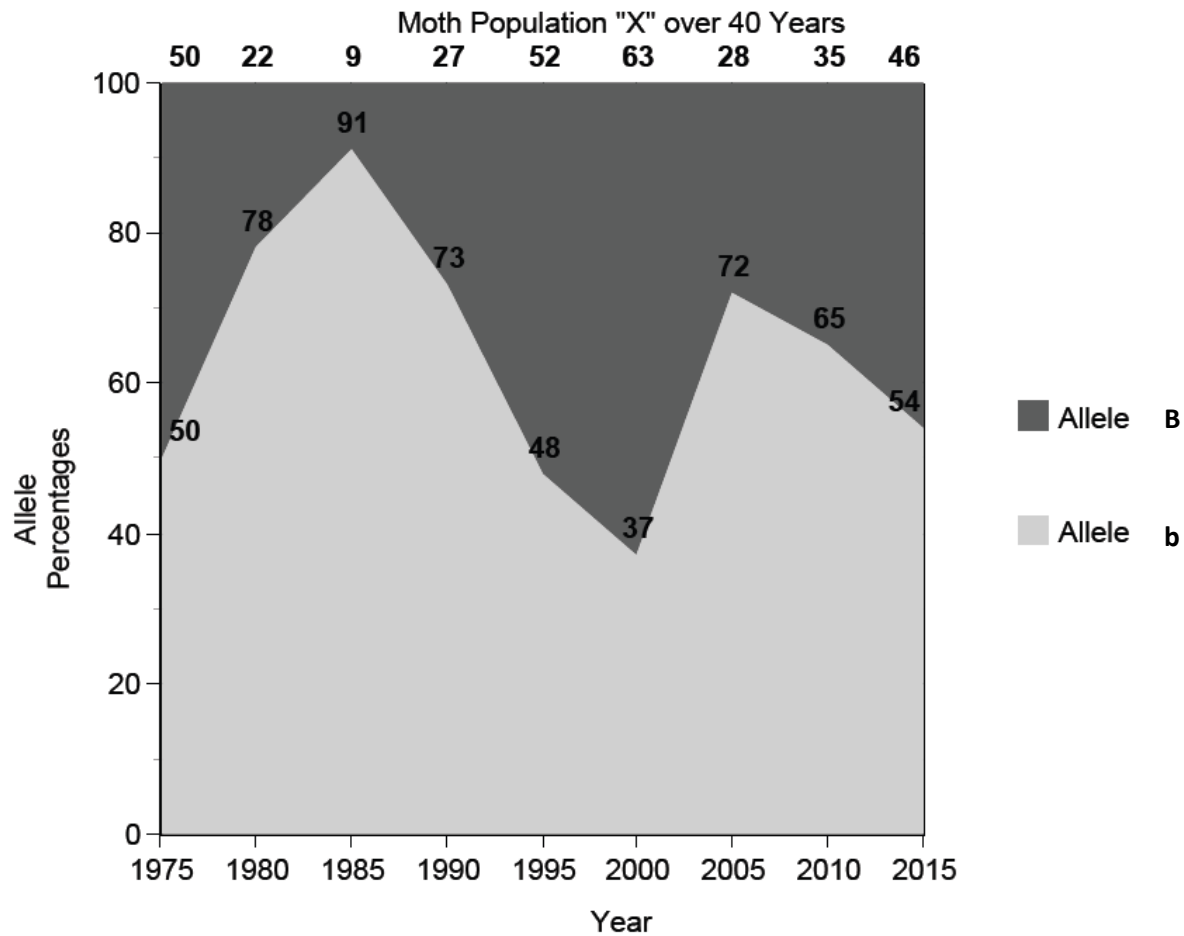
Table 3 – Moth Population “C” over 40 years in USA

	1975	1980	1985	1990	1995	2000	2005	2010	2015
Population Size	100,000	100,254	100,429	100,103	100,642	101,255	101,298	102,055	102,845
Allele B %	10%	17%	27%	42%	48%	49%	50%	50%	50%
Allele b %	90%	83%	73%	58%	52%	51%	50%	50%	50%

Table 4 – Moth Population “D” over 40 years in Japan

	1975	1980	1985	1990	1995	2000	2005	2010	2015
Population Size	100,000	100,254	100,429	100,103	100,642	101,255	101,298	102,055	102,845
Allele B %	0%	0%	3%	16%	28%	32%	39%	25%	15%
Allele b %	100%	100%	97%	84%	72%	68%	61%	75%	85%

Graph the 4 data sets on separate graph paper. You may put the 4 graphs on 1 paper or on separate papers. The x-axis is each year and the y axis will plot Allele "B" percent in one color and allele "b" in a second color, based on 100%. See example below for formatting. The best way to plot the data is to plot the frequency of one allele like a scatterplot and then shade underneath to represent that allele. Next shade the upper region to the top of the graph in a second color. Be sure each graph has a title to demonstrate which population's data it represents.



Null Hypothesis Testing by the Chi Square Test

The Chi Square Test – Tests for a statistically significant difference between outcomes of data that we **observe** by an experiment and those we calculate **expected** values for based on a null hypothesis. This test is great for inheritance pattern verifications & category-based data, but it can be used for many other applications also. After performing the Chi Square test, the value known as χ^2 (Chi-square) will be the number of interest. If the χ^2 value is greater than the critical value in the Chi Square table, we reject the null hypothesis.

1. The null hypothesis that can test if the changes in allele frequencies for the moth population A (table 1) are significant and caused by a specific mechanism is:

There will be no change in the allele frequencies (dominant or recessive) over the generations.

Use the null hypothesis & the initial generation year (1975) to discuss what the **expected** values should be.

2. Complete the table below to calculate the chi square value.

Categories	Observed values	Expected values	O-E	$(O-E)^2$	$\frac{(O-E)^2}{E}$	
1980						
1985						
1990						
1995						
2000						
2005						
2010						
2015						
					SUM of ALL =	$=\chi^2$

3. Critical values are listed in a provided Chi Square Table on your formula sheet. The critical value is always at **the p= 0.05 row** and degrees of freedom is determined by the number of categories minus 1. Make a decision about the null hypothesis and explain the results in terms of evolution mechanisms.

Questions: Answer on the pages with your graphs in complete sentences.

1. Which population shows either a mutation occurred or a migration occurred? Explain your answer.
2. Which population shows genetic drift occurring? Explain your answer using 2 pieces of evidence from the data.
3. The color of moths is controlled by the B/b alleles. The 2 alleles are actually incompletely dominant and the heterozygote (Bb) forms a blend of colors in males that are preferred by females over either of the homozygous varieties (BB or bb). This phenomenon is called "Heterozygote Advantage", where the heterozygote has some mating advantage in the population. Which population is this reflecting and which mechanism of evolution is causing it?
4. In Ireland (population "B") the climate can usually fluctuate but over these 40 years it was much colder than average. The "B" allele codes for a black color and the "b" allele codes for a white color. Darker colors absorb more solar energy and thus heat. Use the data and this scenario to explain why the population allele frequencies changed over generations and how it demonstrates natural selection by survival of the fittest.